

FIG. 1A(1)

10 30 50 70
gaattccggcgagtgaggcgctgacagggactcgcgggggcattcttgacagagccccctggaccacgcccgcctatgcagcctccag 90 110 130 150 170
ccagtcctctctctgcgcgtctctcctcgccatggaggccgcgcgaccgcgctccgcgggcttcgagcagcgagccggcgccgggct 190 210 230 250
gaccccatgtggcgagagcccggtcctgagcgaggctgcgctgcgctcccccgcggtcccgccccccagcgccgggctcggt 270 290 310 330
cagcatggattcctgttcattctgtcctgttggcagtggtctaatacatatgtagtgccaacaatgctactacagtttcacc 350 370 390 410
M D S W F I L V L F G S G L I H V S A N N A T T V S P
ttcttttaggaacgacagattaataaaacatcaacaacagaattggctaaggagagaataaaacctcaaatccaacctcttc 430 450 470 490
S L G T T R L I K T S T T E L A K E E N K T S N S T S S
agtaattctcttctgtggcaccacattcagccccaaacctgactctggagccccacctatgtgactactgttaattcttcaca 510 530 550 570
V I S L S V A P T F S P N L T L E P T Y V T T V N S S H
ctctgacaaatgggaccagggcgagccagcacgggaattctggaggcactaccatttccccgaaacggaagctggcttattgagaa 590
S D N G T R R A A S T E S G G T T I S P N G S W L I E N
ccagttcacggatgccataacagaaacctgggagggggaactccagcactgcagcaacctactccagaaacctccccccggcaga 610 630 650 670
Q F T D A I T E P W E G N S S T A A T T P E T F P P A D
tgagacaccaattattgcggtgatggcgccctgtcctctctgtagtaactcgtgtttattatcatagttctgtacatgttaag 690 710 730 750
E T P I I A V M V A L S S L L V I V F I I I V L Y M L R
gtttaagaaatacaagagctgggagtcattcccaactcttccgctgtcaaatggccgcagcgaggatgtggagccccaaag 770 790 810 830
F K K Y K Q A G S H S N S F R L S N G R T E D V E P Q S
tgtaccacttctggccaggtccccgagcaccaacaggaagtaccaccactgcctgtggacaagctggagagagagattaaaccg 850 870 890 910
V P L L A R S P S T N R K Y P P L P V D K L E E E I N R
gagaatggctgatgacaataagctcttcagagaagaattcaacgctctccctgctgttcctatccagggccacctgtgaggctgc 930 950 970 990 1010
R M A D D N K L F R E E F N A L P A C P I Q A T C E A A

FIG. 1A(2)

ctccaagggaagaaacggaacccgctatgttaaaccatcctgcctctatgaccactctagagtgccactgacacctgttg
S K E E N K E [K N R Y V N I L P Y D H S R V H L T P V E 1030 1050 1070 1090
1110
aagggtcccagattctgattacatcaacgcttcattcattaatggctaccaggaagaaagaacaaattcctgcctgcacaaggac
G V P D S D Y I N A S F I N G Y Q E K N K F I A A Q G P E 1150 1170
1130
caaaagaagaacagtgactctctggagaatgatatgggaacaaaacacagctactattgtcatgttgaccaacctgaagg
K E E T V N D F W R M I W E Q N T A T I V M V T N L K E 1230 1250
1210
agagaaggagtgtaaatgtgccccactgcccagaccaaggctgctggacctatgggaatgtcctgtgtctgtcgaggatg
R K E C K C A Q Y W P D Q G C W T Y G N V R V S V E D V 1330 1430
1370
tgactgttctggactacacagtacggaattctcgatccagcaggtggcgacgtgaccaacaggaacacacagcgcctcat
T V L V D Y T V R K F S I Q Q V G D V T N R K P Q R L I 1450 1470 1490 1510
1410
cactcagttccacttcaccagctggccagactttgggtgcctttcaccccaattggcatgctcaagttcctcaagaagtggaag
T Q F H F T S W P D F G V P F T P I G M L K F L K K V K 1530 1550 1570 1590
gcctgtaacctcagtcagcaggggctatcgtgttcactgcagtcaggtgtaggcgactggcacccttgtgttcctcgtatg
A C N P Q Y A G A I V V H C S A G V G R T G T F V V I D A 1610 1630 1650 1670
ccatgctggacatgatgcattcggagcgcaagtggtatgtatgggttgtgagccggatccggcagcgtgccagatggta
M L D M M H S E R K V D V Y G F V S R I R A Q R C Q M V 1690 1710 1730 1750
cagacagacatgcagtacgtcttcataaccaggcccttctggagcattatctgtatgggacacagaaactggaagtgaacttc
Q T D M Q Y V F I Y] Q A L L E H Y L Y G D T E L E V T S L 1770
1790
tagaaacccacctacaaaaattataacaagatcccaggactagcaacaacgggttagaggaggttaagaaattaacttc
E T H L Q K I Y N K I P G T S N N G L E E F K K L T S 1810 1830 1850
1870
aatcaaatccagaatgacaagatgcgcacgggaacccctccagcccaacatgaagaagacgggttagaggaggttaagaaattaacttc
I K I Q N D K M R T G N L P A N M K [K N R V L Q I I P Y 1890 1910 1930
1950
gaatttaacagagtgcattccagtcacaaacgagcggaagacagacagactatgtgaacgcattccttcattgatggataccggc
E F N R V I I P V K R G E N T D Y V N A S F I D G Y R Q 1970 1990 2010

FIG. 1B

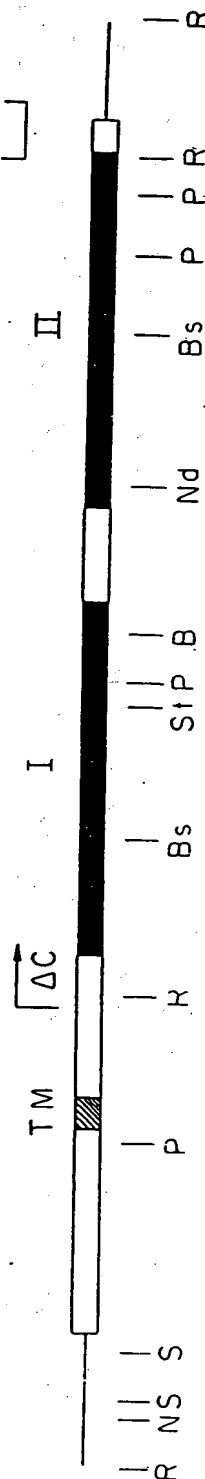


FIG. 2

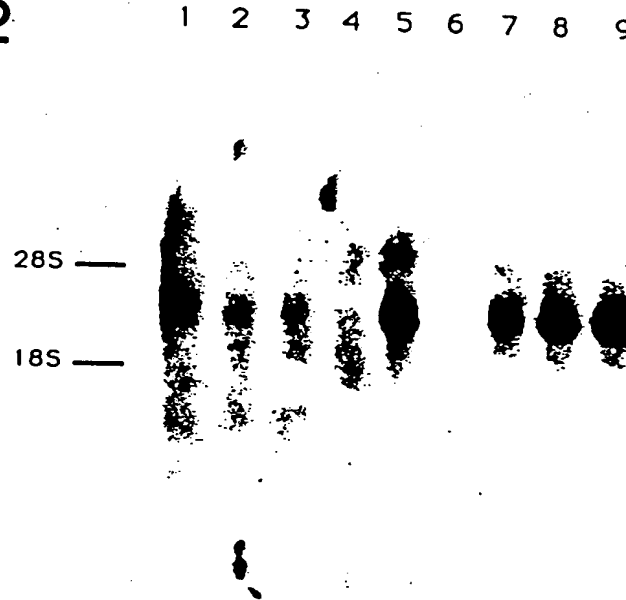
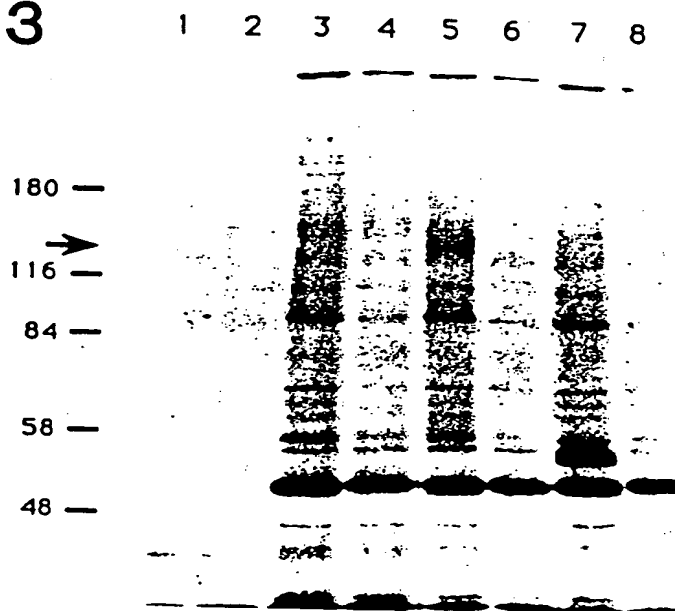


FIG. 3



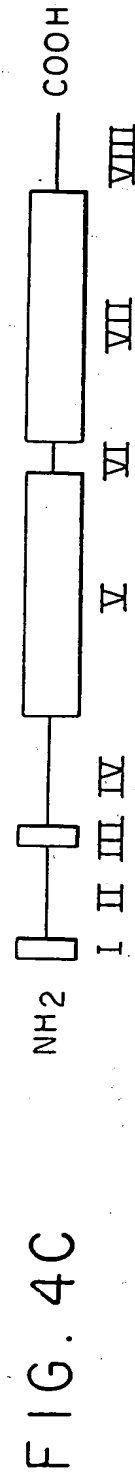
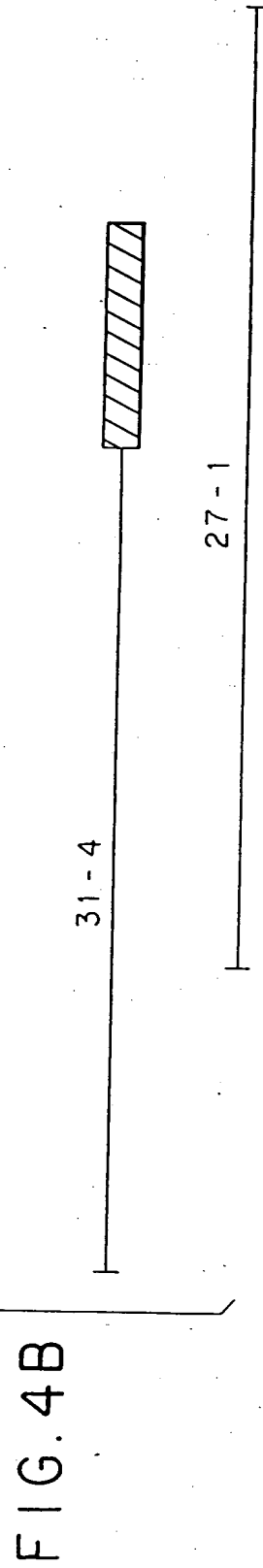
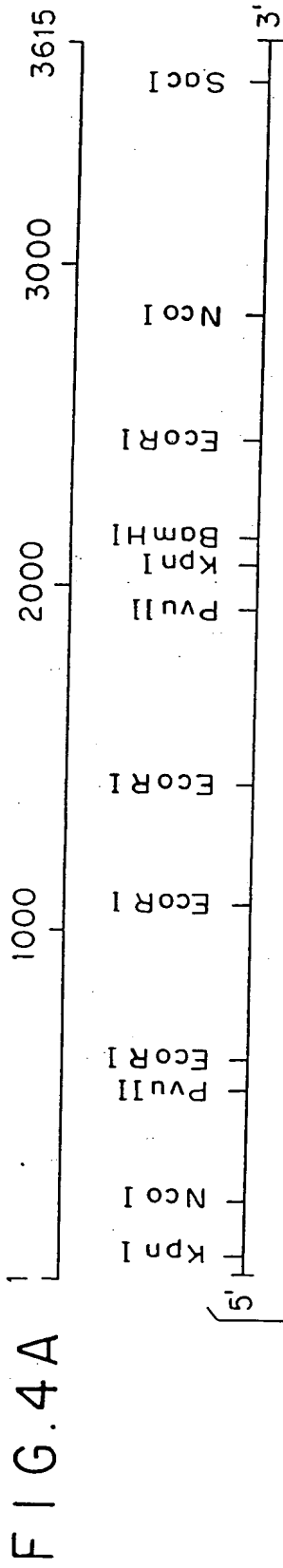


FIG. 5A

	10	20	30	40		
LCA	NqnKNRYVdILPYDynRVeL	sEinGdagSnYINASyIdGfkEprKyIAA				
RPTPase α	NKeKNRYVNILPYDIISRVhLtpvE	GvpdSDYINASfInGYqEknKfIAA				
RPTPase β	NKHKNRYINiVAYDHSRVKLaqLaeKDgKltDYINANYVDGYNrpKAYIAA					
RPTPase γ	NKHKNRYINiLAYDHSRVKLrpLpgKDsKhsDYINANYVDGYNkaKAYIAA					
CON	NkhKNRY-nIl-YDhsRVkL--l--k--k-sdYINA-y-dGynepk-yIAA					
	50	60	70	80	90	
LCA	QGPrdETVdDFWRMIWEQkatvIVMVTrceEgnrnKCAeYWPsmEegTra					
RPTPase α	QGPkeETVnDFWRMIWEQntatIVMVtNLKerkeCKCAQYWPdqGewTYG					
RPTPase β	QGPLKSTaEDFWRMIWEhNvevIVMITNLVEKGRRKCDQYWPdGSEEGY					
RPTPase γ	QGPLKSTfEDFWRMIWEqNtgiIVMITNLVEKGRRKCDQYWptenSEEGY					
CON	QGPLk-TveDFWRMIWEqnt-vIVM-TnlvEkgrrrKC-qYWP--gse-yg					
	100	110	120	130		
LCA	fgdVvVkinghkrcpDYiiqKl	nIvn	kkekatgRevThiq			
RPTPase α	NirVsVedVtVLv	DYTVRKFc	IQqvGd	mtnRkpgRliTQfh		
RPTPase β	NflVTqKSVqVLA	yYTVRnFtlRNTKIKK	Gs	qKGRpsgRVVTQYH		
RPTPase γ	NiiVTlKStkihAc	YTVRrFsiRNTKvKK	GqkgnpKGRqneRVViQYH			
CON	ni-Vtvk-v-vla--dytvrkf--rntki-k-g-k---kgr--gRvvtqyh					
	140	150	160	170	180	190
LCA	FTSWPDhGVPedPhllLKlrrrVnAfsnffsGpIVVHCSAGVGRTGTyigID					
RPTPase α	FTSWPDfGVPftPigmLKFlkKvKAcnpqyaGaIVVHCSAGVGRTGTfvVID					
RPTPase β	YTQWPDmGVPEYsLPVLTfVRKaayAkrhavGPVVHCSAGVGRTGTyIVId					
RPTPase γ	YTQWPDmGVPEYALPVLTfVRrssaArmpetGPVlVHCSAGVGRTGTyIVId					
CON	-T-WPDmGVPeypIplvL-fvr-v-aa-----Gp-vVHCSAGVGRTGTyivId					
	200	210	220	230		
LCA	AMLegleaEnKVDVYGyVvklRrQRClMVQveaQYilIhQALvE					
RPTPase α	AMLdmhhtErKVDVYGfVsRIRaQRcQMVQtdmQYVFiyQALL					
RPTPase β	SMLQQIqhEgTVNifGFLKHIRsQRNYLVQTEEQYVFIHDtLvE					
RPTPase γ	SMLQQIkdkSTVNvlGFLKHIRtQRNYLVQTEEQYiFIHDaLLE					
CON	-MLqqi--e--v-vyGf-khiR-QR-y-VQteeQY-fIH-aL-E					

FIG. 5B(1)

	10	20	30	40	
LCA	NksKNRnsnvIPYdyNRVplkhelemskesehdsdssdddsEEpskY				
RPTase α	NmkKNRvlqIIPYefNRViIpkvr			GEEnTDY	
RPTase β	NrEKNRtSSIIPvERSRVGIssLs			GE GTDY	
RPTase γ	NkEKNRnSSvvPseRaRVGlapLp			GmkGTDY	
CON	NkeKNRnss-iPyernRVg---	l-----	geegtdY		
	50	60	70	80	90
LCA	iNASFImsYwkpevmIAaQGPLkeTigDFWqMifqrKvkviVMLTELkhg				
RPTase α	vNASFIIdGYrQkdsyIASQGPLLHTIeDFWRMIWewKscsIVMLTELeer				
RPTase β	INASYIMGYYSNEFIITQHPLLHTIKDFWRMIWDHNAQlVVMiPDgQnm				
RPTase γ	INASYIMGYYSNEFIITQHPLpHTtKDFWRMIWDHNAQiivMLPDnQsl				
CON	iNAS-ImgYyqsnefi-tQ-PLlhTikDFWrMIwdh-naqiVml---	q--			
	100	110	120	130	140
LCA	dQEiCAQYW geGkqtYGDIEvDLKdtdksstYTl RvfelrhskrkdsRtv				
RPTase α	gQEkCAQYWpsdGlvsYGDItVeLKkeeeCESYTV RdllvtntrenkSRqi				
RPTase β	A EDEFVYWPn kDEpi NCESFkVTLmaeehkCLSNEEKli				
RPTase γ	A EDEFVYWPs reEsm NCEaFtVTLiskdrlCLSNEEqii				
CON	aE-e--qYWps-g---	ygd--v-lk---nces-tvt---	e-r-clsn-e-r-i		
	150	160	170	180	
LCA	yQY qY tnWsvEqLP aepKeliSmIqvVkkQklpQk				
RPTase α	rQf HF hgWpEvgiP SdgKgmISiIaaV Qk Qk				
RPTase β	IQDFILEATQDDYVLEVRHFQCPKWPNPDSPIskTFELISVI			K	
RPTase γ	IhDFILEATQDDYVLEVRHFQCPKWPNPdAPISsTFELInVI			K	
CON	iqdfileatqddyvlevrhfgcpkwpnpd-Pis-t-elIsvI-----	qk			

FIG. 5B(2)

	190	200	210	220	230
LCA	nsseGNkhkhk	stPllihCrdGsqqTG	iFCALLnlLE	saetEevvDiFQv	VKa
RPTPase α	qqsGNh	PitVHCsaGagrTGTFCAL	stVLErvkaEgildV	FQtVKs	
RPTPase β	EEAaNR	DGPmIVHDEhGgVtAGTFCAL	TTLmhQLEKENSVD	VyQVAKM	
RPTPase γ	EEAltr	DGPtIVHDEyGaVsAGmlCAL	TTLsqQLEnENaVD	VfQVAKM	
CON	-eea-nr---	dgP-ivH-e-Gav--	GtfcALttlleqle-	En-vDvfQv-Km	
	240	250			
LCA	LrkaRPgMVstfEQYqFLy	dVias			
RPTPase α	LaLqRPhMVgTlEQYeFcYK	Vvqe			
RPTPase β	INLMRPGVFADIEQYQFLYK	ViLS			
RPTPase γ	INLMRPGVFtDIEQYQFIYK	arLS			
CON	-nlmRPg----	iEQYqFLYkvils			

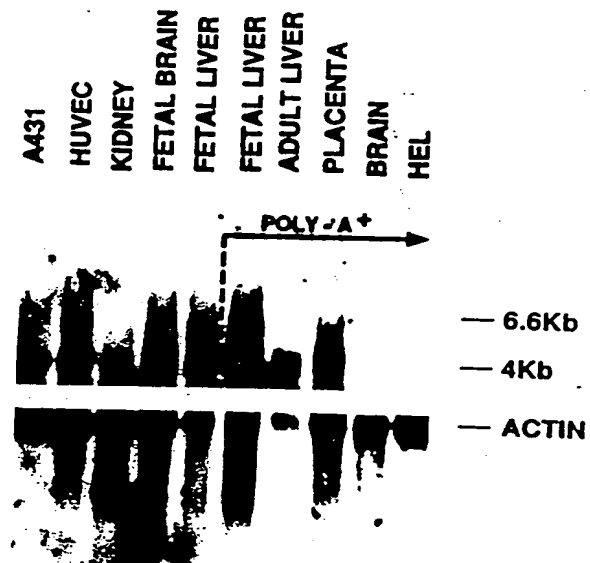


FIG. 6

FIG. 7

HUMAN CHROMOSOMES

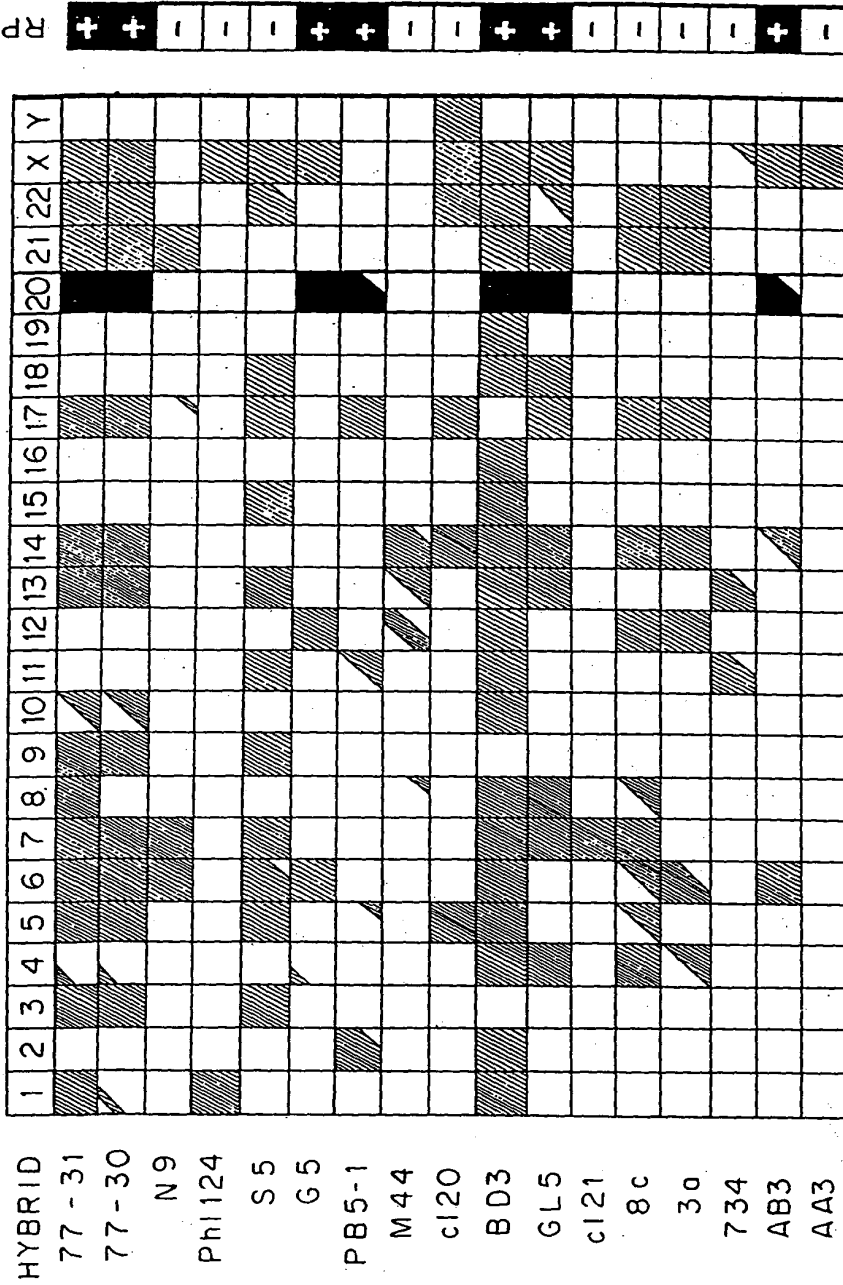


FIG. 8 (1)

1	ATGGATTCTGGTTCATTCTGTTCTGCTCGGCAGTGGTCTGATATGTGTCAAGTCCAAC	60
1	M D S W F I L V L L G S G L I C V S A N	20
61	AATGCTACCACAGTTGCACCTTCTGTAGGAATTACAAGATTAATTAACATCAACGGCA	120
21	N A T T V A P S V G I T R L I N S S T A	40
121	GAACCAGTTAAAGAAGAGGCCAAAACCTTCAAATCCAACCTTCTTCACTAACTTCTCTTTCT	180
41	E P V K E E A K T S N P T S S L T S L S	60
181	GTGGCACCAACATTCAGCCCAAATATAACTCTGGGACCCACCTATTTAACCACCTGTCAAT	240
61	V A P T F S P N I T L G P T Y L T T V N	80
241	TCTTCAGACTCTGACAATGGGACCACAAGAACAGCAAGCACCAATTCTATAGGCATTACA	300
81	S S D S D N G T T R T A S T N S I G I T	100
301	ATTTACCAAATGGAACGTGGCTTCCAGATAACCAGTTCACGGATGCCAGAACAGAACCC	360
101	I S P N G T W L P D N Q F T D A R T E P	120
361	TGGGAGGGGAATTCCAGCACCGCAGCAACCACTCCAGAACTTTCCCTCCTTCAGGTAAT	420
121	W E G N S S T A A T T P E T F P P S G N	140
421	TCTGACTCGAAGGACAGAAGAGATGAGACACCAATTATTGCGGTGATGGTGGCCCTGTCC	480
141	S D S K D R R D E T P I I A V M V A L S	160
481	TCTCTGCTAGTGATCGTGTATTATTATCATAGTTTTGTACATGTTAAGGTTTAAGAAATAC	540
161	S L L V I V F I I I V L Y M L R F K K Y	180
541	AAGCAAGCTGGGAGCCATTCCAATTCTTTCCGCTTATCCAACGGCCGCACTGAGGATGTG	600
181	K Q A G S H S N S F R L S N G R T E D V	200
601	GAGCCCCAGAGTGTGCCACTTCTGGCCAGATCCCCAAGCACCAACAGGAAATACCCACCC	660
201	E P Q S V P L L A R S P S T N R K Y P P	220
661	CTGCCCCGTGGACAAGCTGGAAGAGGAAATTAACCGGAGAATGGCAGACGACAATAAGCTC	720
221	L P V D K L E E E I N R R M A D D N K L	240
721	TTCAGGGAGGAATTCAACGCTCTCCCTGCATGTCCTATCCAGGCCACCTGTGAGGCTGCT	780
241	F R E E F N A L P A C P I Q A T C E A A	260
781	TCCAAGGAGGAAAACAAGGAAAAAATCGATATGTAAACATCTTGCCTTATGACCACTCT	840
261	S K E E N K E K N R Y V N I L P Y D H S	280

FIG. 8 (2)

841	AGAGTCCACCTGACACCGGTTGAAGGGGTTCCAGATTCTGATTACATCAATGCTTCATTC	900
281	R V H L T P V E G V P D S D Y I N A S F	300
901	ATCAACGGTTACCAAGAAAAGAACAAATTCATTGCTGCACAAGGACCAAAAGAAGAAACG	960
301	I N G Y Q E K N K F I A A Q G P K E E T	320
961	GTGAATGATTTCTGGCGGATGATCTGGGAACAAACACAGCCACCATCGTCATGGTTACC	1020
321	V N D F W R M I W E Q N T A T I V M V T	340
1021	AACCTGAAGGAGAGAAAGGAGTGCAAGTGCGCCAGTACTGGCCAGACCAAGGCTGCTGG	1080
341	N L K E R K E C K C A Q Y W P D Q G C W	360
1081	ACCTATGGGAATATTCGGGTGTCTGTAGAGGATGTGACTGTCTGGTGGACTACACAGTA	1140
361	T Y G N I R V S V E D V T V L V D Y T V	380
1141	CGGAAGTTCTGCATCCAGCAGGTGGGCGACATGACCAACAGAAAGCCACAGCGCCTCATC	1200
381	R K F C I Q Q V G D M T N R K P Q R L I	400
1201	ACTCAGTTCCACTTTACCAGCTGGCCAGACTTTGGGGTGCCTTTTACCCCGATCGGCATG	1260
401	T Q F H F T S W P D F G V P F T P I G M	420
1261	CTCAAGTTCCTCAAGAAGGTGAAGGCCTGTAACCCTCAGTATGCAGGGGCCATCGTGGTC	1320
421	L K F L K K V K A C N P Q Y A G A I V V	440
1321	CACTGCAGTGCAGGTGTAGGGCGTACAGGTACCTTTGTCTGTCATTGATGCCATGCTGGAC	1380
441	H C S A G V G R T G T F V V I D A M L D	460
1381	ATGATGCATACAGAACGGAAGGTGGACGTGTATGGCTTTGTGAGCCGGATCCGGGCACAG	1440
461	M M H T E R K V D V Y G F V S R I R A Q	480
1441	CGCTGCCAGATGGTGCAAACCGATATGCAGTATGTCTTCATATACCAAGCCCTTCTGGAG	1500
481	R C Q M V Q T D M Q Y V F I Y Q A L L E	500
1501	CATTATCTCTATGGAGATACAGAACTGGAAGTGACCTCTCTAGAAACCCACCTGCAGAAA	1560
501	H Y L Y G D T E L E V T S L E T H L Q K	520
1561	ATTTACAACAAAATCCCAGGGACCAGCAACAATGGATTAGAGGAGGAGTTTAAGAAGTTA	1620
521	I Y N K I P G T S N N G L E E E F K K L	540
1621	ACATCAATCAAAATCCAGAATGACAAGATGCGGACTGGAAACCTTCCAGCCAACATGAAG	1680
541	T S I K I Q N D K M R T G N L P A N M K	560
1681	AAGAACCGTGTTTTACAGATCATTCATATGAATTCAACAGAGTGATCATTCCAGTTAAG	1740
561	K N R V L Q I I P Y E F N R V I I P V K	580

FIG. 8 (3)

1741	CGGGGCGAAGAGAATACAGACTATGTGAACGCATCCTTTATTGATGGCTACCGGCAGAAG	1800
581	R G E E N T D Y V N A S F I D G Y R Q K	600
1801	GACTCCTATATCGCCAGCCAGGGCCCTCTTCTCCACACAATTGAGGACTTCTGGCGAATG	1860
601	D S Y I A S Q G P L L H T I E D F W R M	620
1861	ATCTGGGAGTGGAAATCCTGCTCTATCGTGATGCTAACAGAACTGGAGGAGAGAGGCCAG	1920
621	I W E W, K S C S I V M L T E L E E R G Q	640
1921	GAGAAGTGTGCCCAGTACTGGCCATCTGATGGACTGGTGTCTATGGAGATATTACAGTG	1980
641	E K C A Q Y W P S D G L V S Y G D I T V	660
1981	GAAGTGAAGAAGGAGGAGGAATGTGAGAGCTACACCGTCCGAGACCTCCTGGTCCACCAAC	2040
661	E L K K E E E C E S Y T V R D L L V T N	680
2041	ACCAGGGAGAATAAGAGCCGGCAGATCCGGCAGTTCCACTTCCATGGCTGGCCTGAAGTG	2100
681	T R E N K S R Q I R Q F H F H G W P E V	700
2101	GGCATCCCCAGTGACGGAAAGGGCATGATCAGCATCATCGCCGCCGTGCAGAAGCAGCAG	2160
701	G I P S D G K G M I S I I A A V Q K Q Q	720
2161	CAGCAGTCAGGGAACCAACCCCATCACCGTGCAGTGCAGCGCCGGGGCAGGAAGGACGGGG	2220
721	Q Q S G N H P I T V H C S A G A G R T G	740
2221	ACCTTCTGTGCCCTGAGCACCGTCCCTGGAGCGTGTGAAAGCAGAGGGGATTTTGGATGTC	2280
741	T F C A L S T V L E R V K A E G I L D V	760
2281	TTCCAGACTGTCAAGAGCCTGCGGCTACAGAGGCCACACATGGTCCAGACACTGGAACAG	2340
761	F Q T V K S L R L Q R P H M V Q T L E Q	780
2341	TATGAGTTCTGCTACAAGGTGGTGCAGGAGTATATTGATGCATTCTCAGATTATGCCAAC	2400
781	Y E F C Y K V V Q E Y I D A F S D Y A N	800
2401	TTCAAGTAA	2409
801	F K *	803